CLAIMS

What is claimed is:

1. A method of simultaneously determining the alleles present in at least two loci from one or more DNA samples, comprising:

a. obtaining at least one DNA sample to be analyzed, wherein the DNA sample has at least two loci which can be amplified together;

b. amplifying the short tandem repeat sequences in the DNA sample; and

c. evaluating the amplified fragments to determine the alleles present at each amplified locus within the DNA sample.

2. The method of claim 1 wherein at least one of the loci is selected from the group consisting of: HUMCSF1PO, HUMTPOX, HUMVWFA31, HUMFESFPS, HUMBFXIII (F13B), HUMLIPOL, HSAC04 (ACTBP2), HUMCYP19, HUMAPOA2, HUMF13A01 and HUMMYOPK (Myotonic).

3. The method of claim 1 wherein at least two loci are selected from the groups consisting of: HUMTH01 and HUMCSF1PO; HUMTH01 and HUMCD4; HUMTH01 and HUMTPOX; HUMF13A01 and HUMFABP; HUMF13A01 and HUMMYOPK (Myotonic); HUMF13A01 and HUMBFXIII (F13B); HUMBFXIII (F13B) and HUMFESFPS; HUMBFXIII (F13B) and HUMLIPOL; HUMHPRTB and HUMFESFPS; HSAC04 (ACTBP2) and HUMCYP19; and HSAC04 (ACTBP2) and HUMFABP.

4. The method of claim 1 wherein the loci are selected from the group consisting of: HUMTH01 and HUMCSF1PO; HUMTH01 and HUMCD4; HUMTH01 and HUMTPOX; HUMF13A01 and HUMFABP; HUMF13A01 and HUMMYOPK (Myotonic); HUMF13A01 and HUMBFXIII (F13B); HUMBFXIII (F13B) and HUMFESFPS; HUMBFXIII (F13B) and HUMLIPOL; HUMHPRTB and HUMFESFPS; HSAC04 (ACTBP2) and HUMCYP19; HUMCSF1PO, HUMTPOX, and HUMTH01; HUMHPRTB, HUMFESFPS and HUMVWFA31; HSAC04 (ACTBP2), HUMCYP19 and HUMPLA2A1; HSAC04 (ACTBP2) and HUMFABP; HUMAPOA2, HUMCYP19 and HUMPLA2A1; HUMCD4, HUMCSF1PO and HUMTH01; HUMCYP19, HUMFABP

and HUMPLA2A1; HUMCYP19, HUMHPRTB and HUMPLA2A1; HUMF13A01, HUMFABP and HUMCD4; HUMHPRTB, HUMFESFPS and HUMLIPOL; HUMF13A01, HUMFABP and HUMCD4; HUMHPRTB, HUMBFXIII (F13B) and HUMPLA2A1; HUMHPRTB, HUMBFXIII (F13B) and HUMTPOX; HUMHPRTB, HUMBFXIII (F13B) and HUMFESFPS; HUMCSF1PO, HUMTPOX and HUMCD4; HUMHPRTB, HUMFESFPS and HUMMYOPK (Myotonic). HUMCSF1PO, HUMTH01 and HUMCD4; HUMCSF1PO, HUMTH01 and HUMVWFA31; HUMHPRTB, HUMBFXIII (F13B) and HUMLIPOL; HUMCSF1PO, HUMTPOX, HUMTH01 and HUMVWFA31; HUMHPRTB, HUMFESFPS, HUMBFXIII (F13B) and HUMLIPOL; HUMCSF1PO, HUMTPOX, HUMTH01 and HUMCD4; and HUMCSF1PO, HUMTH01, HUMTPOX and HUMCD4.

5. The method of claim 1 wherein the loci are HUMHPRTB and HUMFESFPS.

6. The method of claim 1 wherein the loci are HUMCSF1PO, HUMTPOX, and HUMTH01.

7. The method of claim 1 wherein the loci are HUMHPRTB, HUMFESFPS, HUMBFXIII (F13B) and HUMLIPOL.

8. The method of claim 1 wherein the loci are HUMCSF1PO, HUMTPOX, HUMTH01 and HUMVWFA31.

9. The method of claim 1 wherein the loci are HUMHPRTB, HUMFESFPS and HUMVWFA31.

10. The method of claim 1 wherein the DNA in step b. is amplified by polymerase chain reduction.

11. The method of claim 8 wherein the process of amplifying short tandem repeat sequences requires primer pairs selected from the group consisting of SEQ ID. NO. 1 and SEQ ID. NO. 2, SEQ ID. NO. 3 and SEQ ID. NO. 4, SEQ ID. NO. 5 and SEQ ID. NO. 6, SEQ ID. NO. 7 and SEQ ID. NO. 8, SEQ ID. NO. 9 and SEQ ID. NO. 10, SEQ ID. NO. 11 and SEQ ID. NO. 12, SEQ ID. NO. 13 and SEQ ID. NO. 14, SEQ ID. NO. 15 and SEQ ID. NO. 16, SEQ ID. NO. 17 and SEQ ID. NO. 18, SEQ ID. NO. 19 and SEQ ID. NO. 20, SEQ ID. NO. 21 and SEQ ID. NO. 22, SEQ ID. NO. 23 and SEQ ID. NO. 24, SEQ ID. NO. 25 and SEQ ID. NO. 26, SEQ ID. NO. 27 and SEQ ID. NO. 28, SEQ ID. NO. 29 and SEQ ID. NO. 30, and SEQ ID. NO. 31 and SEQ ID. NO. 32.

12. The method of claim 1 further comprising adding short tandem repeat allelic ladders containing nucleotide fragments of the same lengths as two or more known alleles for each of the loci and determining the allele content of the DNA sample by comparison with the amplified short tandem repeat fragments for each of the loci.

13. The method of claim 1 wherein the amplified short tandem repeat sequences are compared by polyacrylamide gel electrophoresis.

14. The method of claim 1 wherein the amplified short tandem repeat sequences are compared using silver stain analysis.

15. The method of claim 1 wherein the amplified short tandem repeat sequences are compared by fluorescent analysis.

16. The method of claim 1 further comprising identifying an appropriate set of loci and primers which provide non-overlapping alleles.

17. The method of claim 1 wherein the samples to be tested are selected from the group consisting of blood, semen, vaginal cells, hair, saliva, urine or other tissue, placental cells or fetal cells present in amniotic fluid and mixtures of body fluids.

18. A method of simultaneously determining the alleles present in at least two loci from one or more DNA samples, comprising:

a. identifying an appropriate set of loci and primers which provide non-overlapping alleles;

b. obtaining at least one DNA sample to be analyzed, wherein the DNA sample has at least two loci which can be amplified together;

c. amplifying the short tandem repeat sequences in the DNA sample; and

d. evaluating the amplified fragments to determine the alleles present at each amplified locus

within the DNA sample.

19. A kit for simultaneously analyzing short tandem repeat sequences in at least two loci from one or more DNA samples, comprising:

a. a container containing oligonucleotide primer pairs for each of the specified loci; and

b. instructions for use.

20. The kit of claim 17 wherein the primer pairs are selected from the group of loci consisting of SEQ ID. NO. 1 and SEQ ID. NO. 2, SEQ ID. NO. 3 and SEQ ID. NO. 4, SEQ ID. NO. 5 and SEQ ID. NO. 6, SEQ ID. NO. 7 and SEQ ID. NO. 8, SEQ ID. NO. 9 and SEQ ID. NO. 10, SEQ ID. NO. 11 and SEQ ID. NO. 12, SEQ ID. NO. 13 and SEQ ID. NO. 14, SEQ ID. NO. 15 and SEQ ID. NO. 16, SEQ ID. NO. 17 and SEQ ID. NO. 18, SEQ ID. NO. 19 and SEQ ID. NO. 20, SEQ ID. NO. 21 and SEQ ID. NO. 22, SEQ ID. NO. 23 and SEQ ID. NO. 24, SEQ ID. NO. 25 and SEQ ID. NO. 26, SEQ ID. NO. 27 and SEQ ID. NO. 28, SEQ ID. NO. 29 and SEQ ID. NO. 30, and SEQ ID. NO. 31 and SEQ ID. NO. 32.

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